Amendments to the Specification

Please insert the Sequence Listing submitted herewith in electronic text form and in electronic pdf form.

Please replace the paragraph at page 15, lines 10-17, with the following amended paragraph:

~~(a) This is~~ Fig. 8a shows the determined nucleotide sequence of SNUT (SEQ ID NO: 3) and its complementary sequence (SEQ ID NO: 4), as well as the encoded amino acid sequence (SEQ ID NO: 5). The fragment was cloned into pQE30 using the *Bam*HI site of this vector. When in the wanted orientation, insertion results in the inactivation of the upstream cloning site, therefore allowing any subsequent cloning of target inserts with the downstream *Bam*HI site (see Fig. 8b ~~(b)~~ for restriction map of sequence).

Please replace the paragraph at page 23, lines 8-15, with the following amended paragraph:

Variances in the sequence of the SNUT domain were observed from the sequence for SrtA that has been logged in Genbank (AF162687). The variances are (using the annotation of AF162687) nucleotide 604 AΔG causing an amino acid mutation of KΔR; nucleotide 647 AΔG, codon remains K, therefore a silent mutation; nucleotide 966 GΔA causing an amino acid mutation of GΔQ. The nucleotide and amino acid sequences of AF162687 comprise SEQ ID NOS: 1 and 2, respectively.

Please replace the paragraph at page 40, lines 21-32 and page 41, lines 1-4, with the following amended paragraph:

Based on analysis of the amino acid sequence and predicted structure of $SrtA_{\Delta N}$, it was decided to amplify the region of amino acids 26 to 171 of the SrtA sequence. Amplification was conducted using the forward primer 5' TTTTTTAGATCTAAACCACATATCGAT (SEQ ID NO: 6) and the reverse primer

5' TTTTTTGGATCCATCTAGAACTTCTAC (SEQ ID NO: 7). This product was then digested with *Bgl*I and *Bam*HI and ligated into pQE30 vector which had also been digested with *Bam*HI to form the pSNUT vector. The ligation mix was transformed into TOP10F' cells and single colonies propagated on LB agar containing 100 ug/ml ampicillin. Clones with the srtA fragment in the correct orientation were screened by expression analysis and positive clones identified using the denaturing dot-blot assay described earlier.